means for determining directionality of expression, wherein the product is associated with at least one phenotypic property of a host cell containing the mRNA sequence; and wherein the expression vector is for expression in non-bacterial host cells.

59. (New) The method of claim 58, wherein the RNA comprises:

a catalytic domain that, when expressed as RNA, cleaves an mRNA sequence transcribed from a target nucleic acid; and

binding sequences flanking the catalytic domain for binding the RNA to the mRNA, and/or wherein the means for determining directionality of expression comprises a different non blunt-ended restriction enzyme site at each end of said double-stranded DNA.

60. (New) The method of claim 59, wherein the double-stranded DNA is formed by contacting a first oligonucleotide with a complementary second oligonucleotide, and/or wherein the non blunt-ended restriction enzyme site is complementary to an end of the expression vector.

61. (New) The method of claim 59, wherein said expression vector is formed by: (a) contacting a double-stranded oligonucleotide with an expression vector; or (b) by contacting a single-stranded oligonucleotide with said expression vector; or (c) contacting a triple-stranded oligonucleotide with an expression vector.

62. (New) The method of any one of claim 1, wherein the expression vector is a plasmid or a virus for expression in non-bacterial host cells.

63. (New) The method of claim 62, wherein the virus is a retrovirus or an adeno-associated virus.

64. (New) The method of claim 1, wherein the expression vector is transfected directly into mammalian cells.

65 The method of claim 1, wherein the sample nucleic acid is genomic DNA, cDNA, an expressed sequence tag (EST) or RNA.

66. (New) The method of claim 1, wherein the family contains between 3 and 20 members.

67. (New) The method of claim 1, wherein each member of the family is designed to inhibit the production of a product of the target nucleic acid molecule.

68. (New) The method of claims 1 that is performed in a high throughput format, whereby all members of a family are assessed in a single experiment.

69. (New) The method of claim 1 that is performed in a high throughput format, whereby a plurality of different target nucleic acid molecules and/or sample nucleotide sequences are assessed.

Please replace claim 8 with amended claim 8 as follows:

8. (Amended) A method of assigning a function to a product coded for by a sample nucleotide sequence, said method comprising:

a) without any intervening bacterial cloning steps,, obtaining and expressing one or more members of an oligonucleotide family as individual transcription products in a plurality of recombinant non-bacterial host cells, wherein:

the coding sequences for each individual transcription product encodes an antisense nucleic acid that, when expressed as RNA binds to mRNA transcribed from a target nucleic acid molecule that comprises a nucleotide sequence of the sample nucleic acid; and

expression of one or more of the individual transcription products inhibits production of a product of the mRNA;

b) analyzing phenotypic changes in the resulting host cells to thereby identify one or more altered function(s); and

c) obtaining a nucleotide sequence of said target nucleic acid, whereby, based upon the altered function, a function is assigned to a sample nucleotide sequence.